

960296\_99004\_Seq\_Lst  
SEQUENCE LISTING

<110> Chapman, Edwin R.  
Dong, Min

<120> BOTULINUM NEUROTOXIN B RECEPTORS AND USE THEREOF

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<141> 2003-10-28

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<151> 2002-10-31

<150> 60/498,128  
<151> 2003-08-27

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&lt;223&gt; BoNT/B binding domain

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&lt;223&gt; Gangliosides binding domain or transmembrane domain

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Gly Lys Asn Ala Ile Asn Met Lys Asp Val Lys Asp Leu Gly Lys Thr			
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Met Lys Asp Gln Ala Leu Lys Asp Asp Asp Ala Glu Thr Gly Leu Thr			
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Asp Gly Glu Glu Lys Glu Glu Pro Lys Glu Glu Lys Lys Leu Gly Lys			
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Gly Ile Ile Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr			
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Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Glu Lys Lys Lys Lys			
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Phe Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu			
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Gln Phe Thr Phe Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu			
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Val Met Ala Val Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile			
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Gly Glu Phe Lys Val Pro Met Asn Thr Val Asp Phe Gly His Val Thr			
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Glu Glu Trp Arg Asp Leu Gln Ser Ala Glu Lys Glu Glu Gln Glu Lys			
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Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln Ile  
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Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile Gly  
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Lys Asn Asp Ala Ile Asp Lys Val Phe Val Gly Tyr Asn Ser Thr Gly  
370 375 380

Ala Glu Leu Arg His Trp Ser Asp Ile Leu Ala Asn Pro Arg Arg Pro  
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35

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Gly Lys Arg Leu Lys Lys Lys Thr Thr Ile Lys Lys Asn Thr Leu  
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Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu Val Pro Phe Glu Gln  
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Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Ile  
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Gly Ala Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg  
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Asp	Met	Phe	Ala	Lys	Leu	Lys	Glu	Lys	Phe	Phe	Asn	Glu	Ile	Asn	Lys		
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Tyr	Asp	Lys	Leu	Gly	Lys	Asn	Glu	Ala	Ile	Gly	Lys	Ile	Phe	Val	Gly	
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&lt;400&gt; 7

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Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys  
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Asn Lys Lys Glu Lys Gly Lys Met Lys Asn Ala Met Asn Met Lys  
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Asp Met Lys Gly Gly Gln Asp Asp Asp Ala Glu Thr Gly Leu Thr  
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Glu Gly Glu Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly  
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Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr  
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Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys  
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Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Ala Gly Lys Thr  
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Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile  
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Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu  
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 Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys  
 180 185 190  
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Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile			
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ggg gag gtg aaa gtg ccc atg aac acg gtg gac ctt ggc cag ccc atc			885
Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile			
245	250	255	
gag gaa tgg aga gac cta caa ggc gga gag aag gaa gag cca gag aag			933
Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu Lys			
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Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile			
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acg gag ctg cg <sub>g</sub> cac tgg tcc gac atg ctg gcg aac cct cg <sub>g</sub> agg ccc			1317
Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro			
390	395	400	
atc gcc cag tgg cac tct ctg aag cct gag gaa gaa gtg gat gct ctt			1365
Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala Leu			
405	410	415	
ctg ggc aag aac aag tag gcagcggcgc ctggggccac gccccagagg			1413
Leu Gly Lys Asn Lys			
420			
acactgacga gctccagagc tatcaatacc tcagttatgc gaccttagag gtttcttcat			1473
ttgtttgcgg tgtgtcctgt tttccttcc tttttctttt tttgtctttt taaaaacc			1533
cttccttttg gtggctatgt gaagaggccc ctaagacgtg aaagagaagc ctggctctgt			1593

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tattgtccca	ggagctgtcc	ttgttgcagt	ccctatcacg	gttgc(ccc)tc	accccaga	tg	1653
gggcctcta	ctgtcagagt	ggaagcactt	cctgctttc	ctgggtttg	gaccaaca	aa	1713
gtggcaagca	cattctgtgt	ctcgactgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg		1773
tgtgtgtgtg	tgtgtgtgt	cacgtgtgcc	catccatccc	cacctgcct	ctgtttggaa		1833
tatctcttcg	tttctggaat	gagtcacgga	caatgatgcc	gtgtgagaga	ggaaagtctt		1893
caggtactcc	gaggtgagga	gagcccactg	cttaagtgg	cagaggccag	aagctctcat		1953
agtccttgcg	aaaggccatt	tggaagacgc	aagatgtgat	actggatgt	ttccgaacta		2013
ggaccaaagg	cttgcattgcca	tcccagactc	cctcttgc	gtcatggc	tttccccagg	gt	2073
ggggctttgg	gatcattcat	gaaaataaac	tat	ttactcg	actggtcgga	ttcagccagg	2133
gaccgc	caggatgt	cattcttgc	gacgacatca	aacttgaag	aaacaga	aa	2193
cccttactc	agctctggat	cttgcctcg	tccagtgg	ggcagatgct	tcctccctct		2253
gcagagtaca	agcagtgcgt	tcatttgc	tcacgcacca	tctgttttgc	cctctgtt	tc	2313
ccttttgt	taagtggaaa	aataccatct	gacgata	gt	ttgcaca	gagccagaga	2373
cctattagag	ggatgcttgg	gtgttagtt	cccttgagg	ccaggtaagg	aggagg	gtc	2433
aagaagg	gcgttgg	acagtgacaa	gctagacatt	gcagagctcc	tcacaactcc		2493
tattcctgac	cctctggacc	cttgc	cgtatgg	agccggagta	gcccagg	cg	2553
accttaggag	aggccccgtc	cttcc	ttgc	tttagacagtt	ttc	tcaagaa	2613
acagcgcatt	catttcagat	gggtgg	gaaatgtgc	taagg	tttgc	accctatgtt	2673
cgaaattc							2681

<210> 9  
<211> 422  
<212> PRT  
<213> Rattus norvegicus

<400> 9

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala  
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Leu Ala Pro Ala Ala Pro Ala Asp Asn  
20 25 30

Ser Thr Glu Ser Thr Gly Thr Gly Glu Ser Gln Glu Asp Met Phe Ala  
35 40 45

Lys Leu Lys Asp Lys Phe Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro  
50 55 60

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Pro Trp Ala Leu Ile Ala Met Ala Val Val Ala Gly Leu Leu Leu Leu  
65 70 75 80

Thr Cys Cys Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys  
85 90 95

Asn Lys Lys Glu Lys Gly Lys Met Lys Asn Ala Met Asn Met Lys  
100 105 110

Asp Met Lys Gly Gly Gln Asp Asp Asp Ala Glu Thr Gly Leu Thr  
115 120 125

Glu Gly Glu Gly Glu Gly Glu Glu Lys Glu Pro Glu Asn Leu Gly  
130 135 140

Lys Leu Gln Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr  
145 150 155 160

Val Gly Val Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly  
165 170 175

Thr Ser Asp Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys  
180 185 190

Lys Tyr Glu Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn  
195 200 205

Glu Thr Phe Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr  
210 215 220

Leu Val Met Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile  
225 230 235 240

Ile Gly Glu Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro  
245 250 255

Ile Glu Glu Trp Arg Asp Leu Gln Gly Gly Glu Lys Glu Glu Pro Glu  
260 265 270

Lys Leu Gly Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly  
275 280 285

Lys Leu Thr Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp  
290 295 300

Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile His Leu Met Gln Asn  
305 310 315 320

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Gly Lys Arg Leu Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu  
325 330 335

Asn Pro Tyr Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln  
340 345 350

Ile Gln Lys Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu  
355 360 365

Gly Lys Asn Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr  
370 375 380

Gly Thr Glu Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg  
385 390 395 400

Pro Ile Ala Gln Trp His Ser Leu Lys Pro Glu Glu Glu Val Asp Ala  
405 410 415

Leu Leu Gly Lys Asn Lys  
420

<210> 10  
<211> 419  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (37)..(57)  
<223> BONT/B binding domain

<220>  
<221> MISC\_FEATURE  
<222> (58)..(84)  
<223> Gangliosides binding domain or transmembrane domain

<400> 10

Met Arg Asn Ile Phe Lys Arg Asn Gln Glu Pro Ile Val Ala Pro Ala  
1 5 10 15

Thr Thr Thr Ala Thr Met Pro Ile Gly Pro Val Asp Asn Ser Thr Glu  
20 25 30

Ser Gly Gly Ala Gly Glu Ser Gln Glu Asp Met Phe Ala Lys Leu Lys  
35 40 45

Glu Lys Leu Phe Asn Glu Ile Asn Lys Ile Pro Leu Pro Pro Trp Ala  
50 55 60

960296\_99004\_Seq\_Lst

Leu Ile Ala Ile Ala Val Val Ala Gly Leu Leu Leu Leu Thr Cys Cys  
65 70 75 80

Phe Cys Ile Cys Lys Lys Cys Cys Cys Lys Lys Lys Lys Asn Lys Lys  
85 90 95

Glu Lys Gly Lys Gly Met Lys Asn Ala Met Asn Met Lys Asp Met Lys  
100 105 110

Gly Gly Gln Asp Asp Asp Asp Ala Glu Thr Gly Leu Thr Glu Gly Glu  
115 120 125

Gly Glu Gly Glu Glu Glu Lys Glu Pro Glu Asn Leu Gly Lys Leu Gln  
130 135 140

Phe Ser Leu Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val  
145 150 155 160

Leu Gln Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp  
165 170 175

Pro Tyr Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Tyr Glu  
180 185 190

Thr Lys Val His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe  
195 200 205

Thr Phe Lys Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met  
210 215 220

Ala Ile Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu  
225 230 235 240

Val Lys Val Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu  
245 250 255

Trp Arg Asp Leu Gln Gly Glu Lys Glu Glu Pro Glu Lys Leu Gly  
260 265 270

Asp Ile Cys Thr Ser Leu Arg Tyr Val Pro Thr Ala Gly Lys Leu Thr  
275 280 285

Val Cys Ile Leu Glu Ala Lys Asn Leu Lys Lys Met Asp Val Gly Gly  
290 295 300

Leu Ser Asp Pro Tyr Gly Lys Ile His Leu Met Gln Asn Gly Lys Arg  
305 310 315 320

960296\_99004\_seq\_Lst

Leu Lys Lys Lys Lys Thr Thr Val Lys Lys Lys Thr Leu Asn Pro Tyr  
325 330 335

Phe Asn Glu Ser Phe Ser Phe Glu Ile Pro Phe Glu Gln Ile Gln Lys  
340 345 350

Val Gln Val Val Val Thr Val Leu Asp Tyr Asp Lys Leu Gly Lys Asn  
355 360 365

Glu Ala Ile Gly Lys Ile Phe Val Gly Ser Asn Ala Thr Gly Thr Glu  
370 375 380

Leu Arg His Trp Ser Asp Met Leu Ala Asn Pro Arg Arg Pro Ile Ala  
385 390 395 400

Gln Trp His Ser Leu Lys Pro Glu Glu Val Asp Ala Leu Leu Gly  
405 410 415

Lys Asn Lys